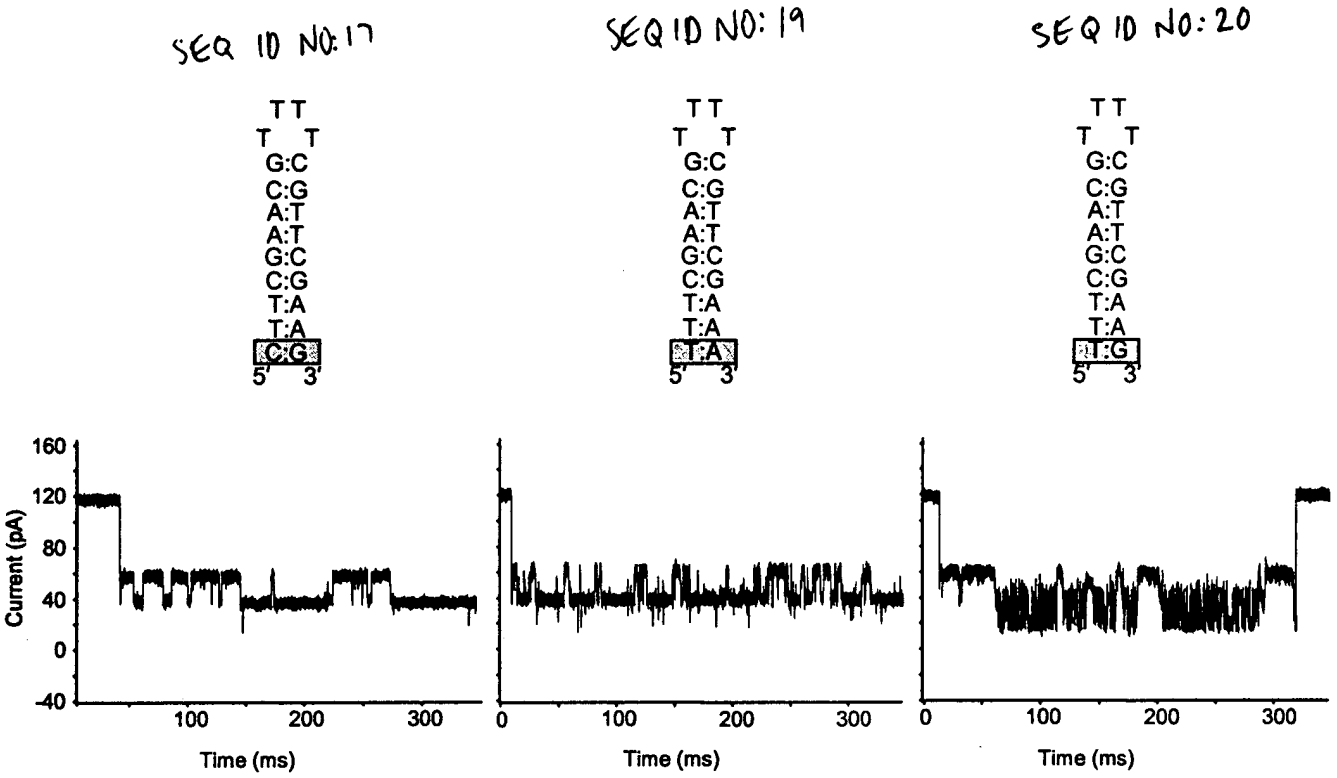

SEQ ID NO: 17
SEQ ID NO: 19
SEQ ID NO: 20
T T
T T
G:C
C:G
A:T
A:T
G:C
C:G
T:A
T:A
C:G
T:A
T:G
5' 3'
Current (pA)
160
120
80
40
0
-40
100
200
300
Time (ms)

Figure 3c

SEQ ID NO:17 SEQ ID NO:19 SEQ ID NO:20

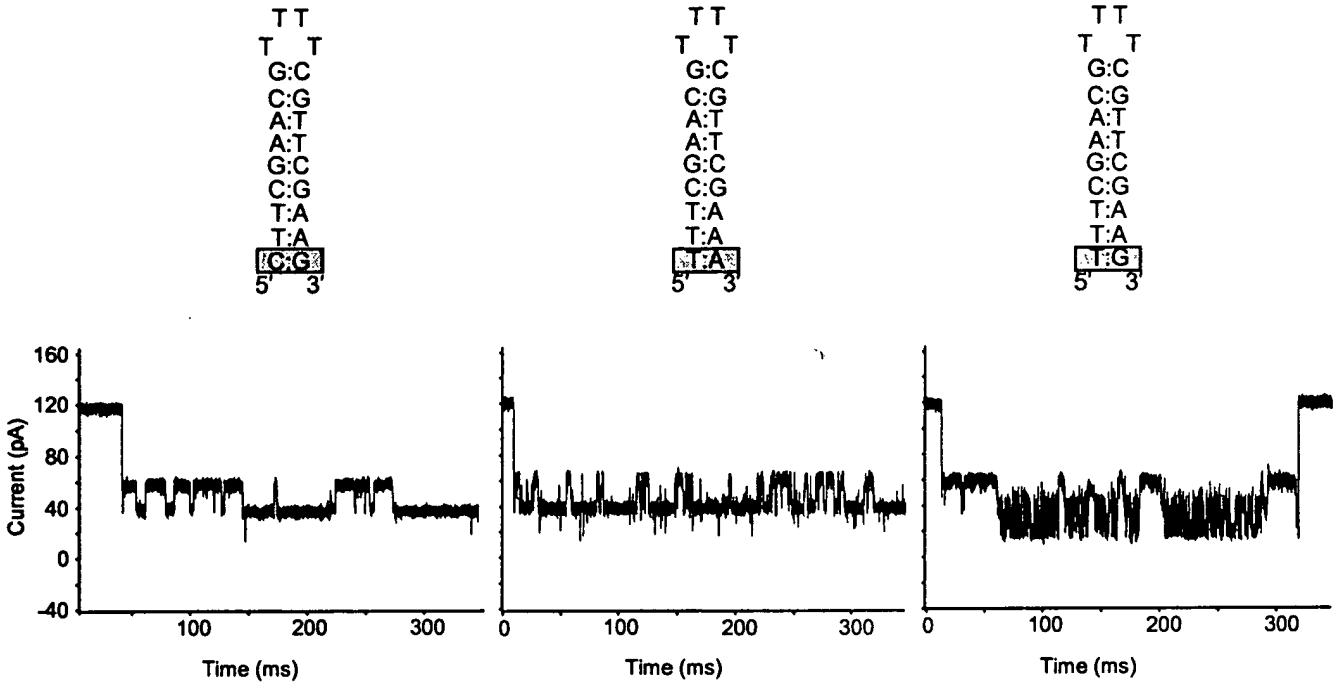
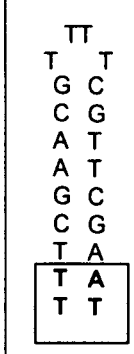
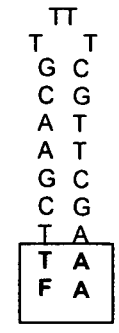
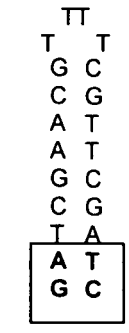
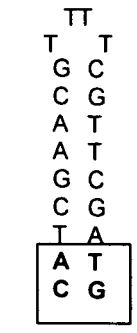
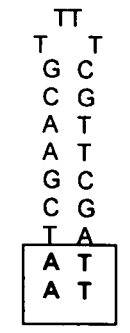
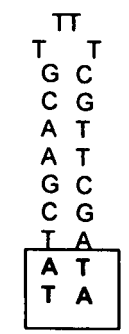


Figure 3c

Figure 8

2

Table X. DNA hairpins used in this study. Primary sequence reads from 5′ end at bottom left to 3′ end at bottom right. Each hairpin has a 9 base-pair-long stem, and a four dT loop. The terminal base-pair and its nearest neighbor are highlighted by a box. These are the base-pairs in closest proximity to the pore limiting aperture when a given hairpin is captured in the α–hemolysin vestibule.

SEQ ID NO: 12	SEQ ID NO: 13	SEQ ID NO: 14	SEQ ID NO: 15	SEQ ID NO: 16	SEQ ID NO: 17	SEQ ID NO: 18	SEQ ID NO: 19	SEQ ID NO: 20	SEQ ID NO: 21	SEQ ID NO: 22
										
9bpGT/CA	9bpCT/GA	9bpAT/TA	9bpTT/AA	9bpTT/GA	9bpTT/TA	9bpFT/AA	9bpGA/CT	9bpCA/GT	9bpAA/TT	9bpTA/AT

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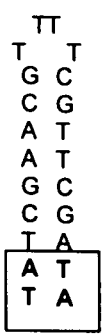
Docket No.: UCAL-199
Application No.: 09/990,102
Applicant: Akeson
CHARACTERIZING DUPLEX NUCLEIC ACID MOLECULES

Figure 8

Table 2. DNA hairpins used in this study. Primary sequence reads from 5′ end at bottom left to 3′ end at bottom right. Each hairpin has a 9 base-pair-long stem, and a four dT loop. The terminal base-pair and its nearest neighbor are highlighted by a box. These are the base-pairs in closest proximity to the pore limiting aperture when a given hairpin is captured in the α–hemolysin vestibule.

SEQ ID NO:12	SEQ ID NO: 13	SEQ ID NO: 14	SEQ ID NO: 15	SEQ ID NO: 16	SEQ ID NO: 17	SEQ ID NO: 18	SEQ ID NO:19	SEQ ID NO: 20	SEQ ID NO: 21	SEQ ID NO: 22
										
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Title: METHODS AND DEVICES FOR CHARACTERIZING DUPLEX NUCLEIC ACID MOLECULES
Applicant: Akeson
Application No.: 09/990,102
Docket No.: UCAL-199
Substitute Figure 8 (Clean Copy)